

WHAT IS CLAIMED IS:

1. A method of detecting a predisposition to allergic bronchopulmonary aspergillosis, said method comprising steps of:
 - (1) designing and synthesizing oligonucleotide primers capable of amplifying Exon 4 of human SP-A2 gene,
 - (2) amplifying genomic DNA of allergic bronchopulmonary aspergillosis patients and normal control individuals using said primers of step (a),
 - (3) sequencing the amplified genomic DNA and identify sequence variations of the amplified genomic DNA computationally by comparing it with an existing sequence of human SP-A2 gene,
 - (4) screening normal control individuals and allergic bronchopulmonary aspergillosis patients for single nucleotide polymorphisms by sequencing of the amplified genomic DNA of the individuals using the said primers of step (a),
 - (5) computing the frequency of G/C haplotypes at 1649 position and A/G haplotypes at 1660 position of allergic bronchopulmonary aspergillosis patients and normal control individuals,
 - (6) establishing the association of G (at 1649 position) and G (at 1660 position) haplotypes with the allergic bronchopulmonary aspergillosis disease based on their frequency distribution in normal individuals and allergic bronchopulmonary aspergillosis patients, and
 - (7) predicting the risk or susceptibility to allergic bronchopulmonary aspergillosis based on the haplotype present at the polymorphic sites in the individual tested, C (at 1649 position) and A (at 1660 position) haplotypes being at low risk and G (at 1649 position) and G (at 1660 position) haplotypes at high risk to the allergic bronchopulmonary aspergillosis.
2. A method as claimed in claim 1 wherein the oligonucleotide primers capable for amplification of said Exon 4 of said SP-A2 gene are selected from the group consisting of:
 - (a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. 1), which is a forward primer, and

(b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. 2), which is a reverse primer.

3. A method as claimed in claim 1 wherein the length of oligonucleotide primers of said oligonucleotide primers is between 5 and 100 bases.

4. A method as claimed in claim 1 wherein, the SP-A2 gene has allelic variants which have G/C and A/G haplotypes.

5. A diagnostic kit for the detection of single nucleotide polymorphisms (G/C at 1649 position and A/G at 1660 position) comprising primers selected from the group consisting of:

(a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. 1), which is a forward primer, and
(b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. 2), which is a reverse primer.

6. Primers suitable for amplification of SP-A2 gene region containing one or more polymorphic sites, said primer selected from the group consisting of:

(a) 5' TGC CTG GAG CCC CTG GTG TCC CTG GAG AGC 3' (SEQ. ID. No. 1), which is a forward primer, and
(b) 5' TGC CTC GTC CGC ATT CAC CCT TCA GAC TGC 3' (SEQ. ID. No. 2), which is a reverse primer.